AMENDMENTS TO THE CLAIMS

Listing of Claims:

1. (currently amended) A method for identifying an ~~agent that has an inhibitory effect on~~ an inhibitor of the complex-formation of an ARE-containing mRNA and an HuR (Hu-Antigen R) protein comprising:
   (a) providing a soluble form of a HuR protein selected from the group of proteins consisting of the amino acid sequences set forth in SEQ ID NO:3 or SEQ ID NO:4, ~~with the proviso that a full-length HuR-glutathione-S-transferase fusion protein is excluded~~,
   (b) providing an ARE-containing mRNA,
   (c) providing a candidate ~~compound~~ inhibitor,
   wherein at least one of (a), (b) and (c) is labeled,
   (d) mixing the HuR protein of step (a) and the ARE-containing mRNA of step (b)
      (i) in the presence of the candidate inhibitor of step (c) and
      (ii) in the absence of the candidate inhibitor of step (c)
      for a sufficient period of time so that the HuR protein of step (a) and the ARE-containing mRNA of step (b) can form a complex,
   (e) detecting the amount of complexes formed in step (d) and/or detect the non-complexed mRNA/protein species,
   (f) comparing the amount of complexes formed in step (d)(ii) ~~and/or~~ with the non-complexed mRNA/protein species formed in step (d)(i) ~~found in the presence and in the absence of (c)~~, and
   (g) ~~choosing an agent which has an influence on the complex formation detected in step (f)~~ identifying a candidate inhibitor that inhibits complex formation between the ARE-containing mRNA and the HuR protein.

2. (original) The method of claim 1 characterized in that the HuR protein is provided as a homogenous solution.

3. (previously presented) The method of claim 1 characterized in that HuR is a soluble form of a recombinant full-length protein or a variant or mutant of a soluble form of a full-length protein.

4. (previously presented) The method of claim 1 characterized in that the mRNA fragment is fluorescently labeled.

5. (currently amended) The method of claim 1 characterized in that the ~~detection method is~~ candidate inhibitor is identified by use of a fluorescence spectroscopic method selected from the group consisting of Single Molecule Spectroscopy, Fluorescence Correlation Spectroscopy, Fluorescence Intensity Distribution Analysis, Steady-State Fluorescence Intensity, Fluorescence Anisotropy and Energy Transfer.

6. (withdrawn from consideration) A screening assay (kit) for identifying an agent that has an inhibitory effect on the complex-formation of an ARE-containing mRNA and an HuR protein comprising as a main component
   (a) a soluble form of a HuR protein, with the proviso that a full-length HuR–glutathione-S-transferase fusion protein is excluded,
   (b) an ARE-containing mRNA, and
   (c) optionally means for detection of the amount of complexes formed between said HuR protein and said ARE-containing mRNA and/or for detection of non-complexed mRNA/protein species.

7. (withdrawn from consideration) A pharmaceutical composition comprising an agent identified by a method according to claim 1 in association with at least one pharmaceutical excipient.

8. (withdrawn from consideration) Use of a pharmaceutical composition according to claim 7, for the treatment of a disorder having an etiology associated with the production of a substance selected from the group consisting of cytokine, growth factor, proto-oncogene or a viral protein, preferably the agent is selected from the group consisting of IL-1, IL-2, IL-3, IL-4, IL-8, GM-CSF, TNF-α, VEGF, AT-R1, Cox-2, c-fos and c-myc.

9. (withdrawn from consideration) A full-length HuR protein of SEQ ID NO:1 or SEQ ID NO:2, wherein the C-terminal amino acid in position 326 is esterified.

10. (withdrawn from consideration) An isolated RNA sequence motif which is the binding site for HuR.